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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/887,569	06/25/2001	Maurice M. Moloney	9369-183

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Toronto, ON M5H 3Y2
CANADA

OIPE
DEC 18 2001
PATENT & TRADEMARK OFFICE

5

CONFIRMATION NO. 8071
FORMALITIES LETTER

OC000000006993235

Date Mailed: 10/30/2001

NOTICE TO FILE MISSING PARTS OF NONPROVISIONAL APPLICATION

12/20/2001 BABRAHA1 00000090 09887569

01 FC:201   370.00 OP
02 FC:205   65.00 OP

FILED UNDER 37 CFR 1.53(b)

Filing Date Granted

An application number and filing date have been accorded to this application. The item(s) indicated below, however, are missing. Applicant is given **TWO MONTHS** from the date of this Notice within which to file all required items and pay any fees required below to avoid abandonment. Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a).

- The statutory basic filing fee is missing.
  Applicant must submit $ 710 to complete the basic filing fee for a non-small entity. If appropriate, applicant may make a written assertion of entitlement to small entity status and pay the small entity filing fee (37 CFR 1.27).
- To avoid abandonment, a late filing fee or oath or declaration surcharge as set forth in 37 CFR 1.16(l) of $130 for a non-small entity, must be submitted with the missing items identified in this letter.
- **The balance due by applicant is $ 840.**

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase PatentIn Software, call (703) 306-2600**
- **For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov**

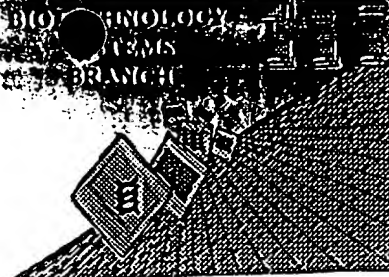*A copy of this notice __MUST__ be returned with the reply.*

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: **09/887,569**

Source: **OIPE**

Date Processed by STIC: **7/7/2001**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker
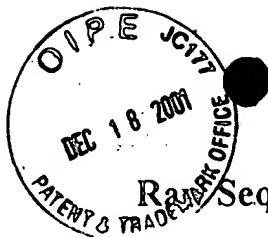
ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/887,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
   ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
   each n or Xaa can only represent a single residue. Please present the maximum number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
   is Artificial Sequence

11 ____ Use of <220>   Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
   "Unknown." Please explain source of genetic material in <220> to <223> section.
   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
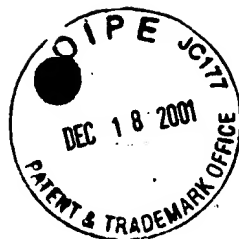
OIPE

RAW SEQUENCE LISTING.
PATENT APPLICATION: US/09/887,569

DATE: 07/07/2001
TIME: 14:35:35

Input Set : A:\SEQUENCE.txt
Output Set: N:\CRF3\07062001\I887569.raw

```
         4 <110> APPLICANT: Moloney, Maurice M.
         5         Habibi, Hamid R.
         7 <120> TITLE OF INVENTION: Expression of Somatotropin in Plant Seeds
         9 <130> FILE REFERENCE: 9369-183
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/887,569
C--> 12 <141> CURRENT FILING DATE: 2001-06-25
        14 <150> PRIOR APPLICATION NUMBER: US 09/210,843
        15 <151> PRIOR FILING DATE: 1998-12-15
        17 <160> NUMBER OF SEQ ID NOS: 2
        19 <170> SOFTWARE: PatentIn Ver. 2.0
        21 <210> SEQ ID NO: 1
        22 <211> LENGTH: 1101
        23 <212> TYPE: DNA
        24 <213> ORGANISM: synthetic construct
        26 <400> SEQUENCE: 1
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        28 atgggccgag accgagacca gtaccagatg tccggacgag gatctgacta ctccaagtct 120
        29 aggcagattg ctaaagctgc aactgctgtc acagctggtg gttccctcct tgttctctcc 180
        30 agccttaccc ttgttggaac tgtcatagct ttgactgttg caacacctct gctcgttatc 240
        31 ttcagcccaa tccttgtccc ggctctcatc acagttgcac tcctcatcac cggttttctt 300
        32 tcctctggag ggtttggcat tgccgctata accgttttct cttggattta caagtacgca 360
        33 acgggagagc acccacaggg atcagacaag ttggacagtg caaggatgaa gttgggaagc 420
        34 aaagctcagg atctgaaaga cagagctcag tactacggac agcaacatac tggtggggaa 480
        35 catgaccgtg accgtactcg tggtggccag cacactactc tcgttccacg aggatccgac 540
        36 aaccagcggc tcttcaataa tgcagtcatt cgtgtacaac acctgcacca gctggctgca 600
        37 aaaatgatta acgactttga ggacagcctg ttgcctgagg aacgcagaca gctgagtaaa 660
        38 atcttccctc tgtctttctg caattctgac tacattgagg cgcctgctgg aaaagatgaa 720
        39 acacagaaga gctctatgct gaagcttctt cgcatctctt ttcacctcat tgagtcctgg 780
        40 gagttcccaa gccagtccct gagcggaacc gtctcaaaca gcctgaccgt agggaacccc 840
        41 aaccagctca ctgagaagct ggccgacttg aaaatgggca tcagtgtgct catccaggca 900
        42 tgtctcgatg gtcaaccaaa catggatgat aacgactcct gccgctgcc ttttgaggac 960
        43 ttctacttga ccatggggga gaacaacctc agagagagct ttcgtctgct ggcttgcttc 1020
        44 aagaaggaca tgcacaaagt cgagacctac ttgagggttg caaattgcag gagatccctg 1080
        45 gattccaact gcaccctgta g 1101
        47 <210> SEQ ID NO: 2
        48 <211> LENGTH: 366
        49 <212> TYPE: PRT
        50 <213> ORGANISM: synthetic construct
        52 <400> SEQUENCE: 2
        53 Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
        54   1               5                  10                  15
        56 Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
        57              20                  25                  30
        59 Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
        60          35                  40                  45
        62 Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
        63      50                  55                  60
```

Does Not Comply Corrected Diskette Needed

see item #10 on ERROR SUMMARY SHEET.

make sure nucleic acid bases are lower case

```
65  Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
66  65                      70                  75                  80
68  Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
69                      85                  90                  95
71  Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
72                  100             105             110
74  Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser
75              115             120             125
77  Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp
78      130             135             140
80  Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu
81  145             150             155             160
83  His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu Val Pro
84              165             170             175
86  Arg Gly Ser Asp Asn Gln Arg Leu Phe Asn Asn Ala Val Ile Arg Val
87              180             185             190
89  Gln His Leu His Gln Leu Ala Ala Lys Met Ile Asn Asp Phe Glu Asp
90          195             200             205
92  Ser Leu Leu Pro Glu Glu Arg Arg Gln Leu Ser Lys Ile Phe Pro Leu
93      210             215             220
95  Ser Phe Cys Asn Ser Asp Tyr Ile Glu Ala Pro Ala Gly Lys Asp Glu
96  225             230             235             240
98  Thr Gln Lys Ser Ser Met Leu Lys Leu Leu Arg Ile Ser Phe His Leu
99              245             250             255
101 Ile Glu Ser Trp Glu Phe Pro Ser Gln Ser Leu Ser Gly Thr Val Ser
102             260             265             270
104 Asn Ser Leu Thr Val Gly Asn Pro Asn Gln Leu Thr Glu Lys Leu Ala
105             275             280             285
107 Asp Leu Lys Met Gly Ile Ser Val Leu Ile Gln Ala Cys Leu Asp Gly
108     290             295             300
110 Gln Pro Asn Met Asp Asp Asn Asp Ser Leu Pro Leu Pro Phe Glu Asp
111 305             310             315             320
113 Phe Tyr Leu Thr Met Gly Glu Asn Asn Leu Arg Glu Ser Phe Arg Leu
114             325             330             335
116 Leu Ala Cys Phe Lys Lys Asp Met His Lys Val Glu Thr Tyr Leu Arg
117             340             345             350
119 Val Ala Asn Cys Arg Arg Ser Leu Asp Ser Asn Cys Thr Leu
120             355             360             365
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VERIFICATION SUMMARY   DATE: 07/07/2001
PATENT APPLICATION: US/09/887,569   TIME: 14:35:36

Input Set : A:\SEQUENCE.txt
Output Set: N:\CRF3\07062001\I887569.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1